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# SEQUENCE LISTING

Millennium Pharmaceuticals, Inc.  
Meyers, Rachel

<120> 27419, A NOVEL HUMAN ARGININE-N-METHYL  
TRANSFERASE AND USES THEREOF

<130> 38155-20039.00

<140> US 09/970,638

<141> 2001-10-03

<150> US 60/237,717

<151> 2000-10-05

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1201

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (34)...(1161)

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Met Ser Gln Pro Lys Lys Arg  
1 5

aag ctt gag tcg ggg ggc ggc ggc gaa gga ggg gag gga act gaa gag 102  
Lys Leu Glu Ser Gly Gly Gly Glu Gly Gly Glu Gly Thr Glu Glu  
10 15 20

gaa gat ggc gcg gag cgg gag gcg gcc ctg gag cga ccc cgg agg act 150  
Glu Asp Gly Ala Glu Arg Glu Ala Ala Leu Glu Arg Pro Arg Arg Thr  
25 30 35

aag cgg gaa cgg gac cag ctg tac tac gag tgc tac tcg gac gtt tcg 198  
Lys Arg Glu Arg Asp Gln Leu Tyr Tyr Glu Cys Tyr Ser Asp Val Ser  
40 45 50 55

gtc cac gag gag atg atc gcg gac cgc gtc cgc acc gat gcc tac cgc 246  
Val His Glu Glu Met Ile Ala Asp Arg Val Arg Thr Asp Ala Tyr Arg  
60 65 70

ctg ggt atc ctt cgg aac tgg gca gca ctg cga ggc aag acg gta ctg 294  
Leu Gly Ile Leu Arg Asn Trp Ala Ala Leu Arg Gly Lys Thr Val Leu  
75 80 85

gac gtg ggc gcg ggc acc ggc att ctg agc atc ttc tgt gcc cag gcc 342  
Asp Val Gly Ala Gly Thr Gly Ile Leu Ser Ile Phe Cys Ala Gln Ala

90	95	100	
ggg gcc cgg cgc gtg tac gcg gta gag gcc agc gcc atc tgg caa cag			390
Gly Ala Arg Arg Val Tyr Ala Val Glu Ala Ser Ala Ile Trp Gln Gln			
105	110	115	
gcc cgg gag gtg gtg cgg ttc aac ggg ctg gag gac cgg gtg cac gtc			438
Ala Arg Glu Val Val Arg Phe Asn Gly Leu Glu Asp Arg Val His Val			
120	125	130	135
ctg ccg gga cca gtg gag act gta gag ttg ccg gaa cag gtg gat gcc			486
Leu Pro Gly Pro Val Glu Thr Val Glu Leu Pro Glu Gln Val Asp Ala			
	140	145	150
atc gtg agc gag tgg atg ggc tac gga ctc ctg cac gag tcc atg ctg			534
Ile Val Ser Glu Trp Met Gly Tyr Gly Leu Leu His Glu Ser Met Leu			
	155	160	165
agc tcc gtc ctc cac gcg cga acc aag tgg ctg aag gag ggc ggt ctt			582
Ser Ser Val Leu His Ala Arg Thr Lys Trp Leu Lys Glu Gly Gly Leu			
	170	175	180
ctc ctg ccg gcc tcc gcc gag ctc ttc ata gcc ccc atc agc gac cag			630
Leu Leu Pro Ala Ser Ala Glu Leu Phe Ile Ala Pro Ile Ser Asp Gln			
	185	190	195
atg ctg gaa tgg cgc ctg ggc ttc tgg agc cag gtg aag cag cac tat			678
Met Leu Glu Trp Arg Leu Gly Phe Trp Ser Gln Val Lys Gln His Tyr			
200	205	210	215
ggg gtg gac atg agc tgc ctg gag ggc ttc gcc acg cgc tgt ctc atg			726
Gly Val Asp Met Ser Cys Leu Glu Gly Phe Ala Thr Arg Cys Leu Met			
	220	225	230
ggc cac tcg gag atc gtt gtg cag gga ttg tcc ggc gag gac gtg ctg			774
Gly His Ser Glu Ile Val Val Gln Gly Leu Ser Gly Glu Asp Val Leu			
	235	240	245
gcc cgg ccg cag cgc ttt gct cag cta gag ctc tcc cgc gcc ggc ttg			822
Ala Arg Pro Gln Arg Phe Ala Gln Leu Glu Leu Ser Arg Ala Gly Leu			
	250	255	260
gag cag gag ctg gag gcc gga gtg ggc ggg cgc ttc cgc tgc agc tgc			870
Glu Gln Glu Leu Glu Ala Gly Val Gly Gly Arg Phe Arg Cys Ser Cys			
	265	270	275
tat ggc tcg gcg ccc atg cat ggc ttt gcc atc tgg ttc cag gtg acc			918
Tyr Gly Ser Ala Pro Met His Gly Phe Ala Ile Trp Phe Gln Val Thr			
280	285	290	295
ttc cct gga ggg gag tcg gag aaa ccc ctg gtg ctg tcc acc tcg cct			966
Phe Pro Gly Gly Glu Ser Glu Lys Pro Leu Val Leu Ser Thr Ser Pro			
	300	305	310
ttt cac ccg gcc act cac tgg aaa cag gcg ctc ctc tac ctg aac gag			1014
Phe His Pro Ala Thr His Trp Lys Gln Ala Leu Leu Tyr Leu Asn Glu			
	315	320	325

ccg gtg caa gtg gag caa gac acg gac gtt tca gga gag atc acg ctg 1062  
 Pro Val Gln Val Glu Gln Asp Thr Asp Val Ser Gly Glu Ile Thr Leu  
 330 335 340  
 ctg ccc tcc cgg cac aac ccc cgt cgc ctg cgc gtg ctg ctg cgc tac 1110  
 Leu Pro Ser Arg His Asn Pro Arg Arg Leu Arg Val Leu Leu Arg Tyr  
 345 350 355  
 aaa gtg gga gac cag gag gag aag acc aaa gac ttt gcc atg gag gac 1158  
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<210> 2  
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 <212> PRT  
 <213> Homo sapiens

<400> 2  
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 Leu Glu Arg Pro Arg Arg Thr Lys Arg Glu Arg Asp Gln Leu Tyr Tyr  
 35 40 45  
 Glu Cys Tyr Ser Asp Val Ser Val His Glu Glu Met Ile Ala Asp Arg  
 50 55 60  
 Val Arg Thr Asp Ala Tyr Arg Leu Gly Ile Leu Arg Asn Trp Ala Ala  
 65 70 75 80  
 Leu Arg Gly Lys Thr Val Leu Asp Val Gly Ala Gly Thr Gly Ile Leu  
 85 90 95  
 Ser Ile Phe Cys Ala Gln Ala Gly Ala Arg Arg Val Tyr Ala Val Glu  
 100 105 110  
 Ala Ser Ala Ile Trp Gln Gln Ala Arg Glu Val Val Arg Phe Asn Gly  
 115 120 125  
 Leu Glu Asp Arg Val His Val Leu Pro Gly Pro Val Glu Thr Val Glu  
 130 135 140  
 Leu Pro Glu Gln Val Asp Ala Ile Val Ser Glu Trp Met Gly Tyr Gly  
 145 150 155 160  
 Leu Leu His Glu Ser Met Leu Ser Ser Val Leu His Ala Arg Thr Lys  
 165 170 175  
 Trp Leu Lys Glu Gly Gly Leu Leu Leu Pro Ala Ser Ala Glu Leu Phe  
 180 185 190  
 Ile Ala Pro Ile Ser Asp Gln Met Leu Glu Trp Arg Leu Gly Phe Trp  
 195 200 205  
 Ser Gln Val Lys Gln His Tyr Gly Val Asp Met Ser Cys Leu Glu Gly  
 210 215 220  
 Phe Ala Thr Arg Cys Leu Met Gly His Ser Glu Ile Val Val Gln Gly  
 225 230 235 240  
 Leu Ser Gly Glu Asp Val Leu Ala Arg Pro Gln Arg Phe Ala Gln Leu  
 245 250 255  
 Glu Leu Ser Arg Ala Gly Leu Glu Gln Glu Leu Glu Ala Gly Val Gly



Lys Gly Gly Glu Glu Asp Phe Glu Gly Leu Leu Gly Glu Gly Tyr Gly  
 50 55 60  
 Ile Thr Gly Glu Tyr Arg Thr Arg Arg Glu Leu Ala Gly Glu Lys  
 65 70 75 80  
 Asp Ser Gly Glu Thr Val Thr Ile His Lys Glu Asn Gly Cys Arg Phe  
 85 90 95  
 Lys Leu Asp Val Ser Lys Val Tyr Phe Ser Pro Arg Leu Glu Gly Glu  
 100 105 110  
 Arg Glu Arg Leu Ala Lys Leu Val Lys Glu Gly Glu Val Val Val Asp  
 115 120 125  
 Met Phe Ala Gly Ile Gly Pro Phe Ser Ile Pro Ile Ala Lys His Ser  
 130 135 140  
 Lys Ala Lys Arg Val Tyr Ala Val Asp Leu Asn Pro Glu Ala Val Lys  
 145 150 155 160  
 Tyr Leu Lys Glu Asn Ile Lys Leu Asn Lys Val Glu Asp Gln Pro Lys  
 165 170 175  
 Ile Gln Thr Val Val Asn Lys Ile Ile Pro Ile Leu Gly Asp Val Arg  
 180 185 190  
 Glu Val Ile Pro Glu Lys Glu Ala Gly Val His Ser Leu Val Lys Leu  
 195 200 205  
 Val Val Ala Asp Arg Val Ile Met Pro Leu Pro Leu Ala Arg Val Gly  
 210 215 220  
 Gln Ile Ser Ala His Glu Phe Leu Asp Lys Ala Leu Arg Lys Val Lys  
 225 230 235 240  
 Asp Gly Gly Ile Leu Val Ser Val Ile His Tyr Tyr Glu Phe Leu Pro  
 245 250 255  
 Glu Lys Ala Ile Pro Phe Leu Pro Val Glu Arg Ile Lys Arg Ala Ala  
 260 265 270  
 Glu Lys Glu Gly Val Lys Val Glu Ile Leu Lys Lys Arg Lys Val Lys  
 275 280 285  
 Asn Tyr Ala Pro Gly Val Tyr His Val Val Leu Asp Ala Arg Val Asn  
 290 295 300

<210> 5

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 5

Pro Asp Lys Cys Thr Leu His Leu Thr Ala Ile Glu Asp Thr Gln Tyr  
 1 5 10 15  
 Lys Asp Glu Lys Ile Asn Phe Trp Asp Asp Val Tyr Gly Phe Asx Met  
 20 25 30  
 Ser Cys Met Lys Asp Ala Ala Ile Lys Glu Pro Ile Val Asp Pro Lys  
 35 40 45  
 Tyr Asn His Val Val Asp Pro Asn Gln Ile Ile Thr Asp Pro Cys Thr  
 50 55 60  
 Ile Lys Glu Phe Asp Met His Thr Val Lys Ile Ser Asp Leu Glu Thr  
 65 70 75 80  
 Phe Thr Ser Pro Phe Lys Leu Thr Val Lys Arg Asn Gly Met Leu His  
 85 90 95  
 Ala Phe Thr Ala Trp Phe Asp Val Tyr Phe Thr Ser Lys Arg Cys His  
 100 105 110  
 Pro Ile Pro Glu Ala Ile Asp Lys Pro Val Gly Phe Ser Thr Gly Pro

115 120 125  
 Gln Ser Pro Tyr Thr His Trp Lys Gln Thr Ile Phe Tyr Met Glu Asp  
 130 135 140  
 Pro Leu Pro Val Lys Thr Gly Asp Thr Ile Glu Gly Ser Ile Thr Ile  
 145 150 155 160  
 Ser Lys Asn Lys Lys Asn Asn Arg Asp Leu Asp Ile Thr Leu Ser Trp  
 165 170 175  
 Asn Val Asn Gly Arg Gln Asp Pro Thr  
 180 185

<210> 6  
 <211> 129  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 6  
 His Ile Arg Met Ile Asn Asp Val Lys Arg Asn Glu Ala Phe Ala Lys  
 1 5 10 15  
 Ala Leu Asn Asp Thr Ile Lys Ser Arg Ile Thr Val Val Phe Asp Ile  
 20 25 30  
 Gly Ser Gly Thr Gly Ile Leu Ser Ala Ile Ala Ala Arg Lys Thr Asn  
 35 40 45  
 Leu Val Thr Ala Leu Glu Glu Asn Met Cys Leu Thr Met Ile Ser Lys  
 50 55 60  
 Glu Val Leu Lys Arg Asn Gly Val Glu Ser Arg Val Asn Val His Ala  
 65 70 75 80  
 Lys Asn Ser Thr Tyr Phe Glu Thr Cys Glu Lys Ala Asp Ile Val Val  
 85 90 95  
 Ser Glu Thr Leu Asp Cys Cys Val Phe Gly Glu Lys Ile Val Glu Thr  
 100 105 110  
 Phe Leu Asp Ala His Val Arg Phe Ser His Asp Arg Thr Ile Phe Ile  
 115 120 125  
 Pro

<210> 7  
 <211> 38  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 7  
 Lys Thr Asp Glu Asp Tyr Tyr Tyr Phe Asp Ser Tyr Ala His Tyr Gly  
 1 5 10 15  
 Ile His Glu Glu Met Leu Lys Asp Ser Val Arg Thr Glu Ser Tyr Arg  
 20 25 30  
 Asp Phe Ile Tyr His Asn  
 35

<210> 8  
 <211> 39  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 8

Gln Asp Glu Glu Tyr Phe Gly Ser Tyr Gly Thr Leu Lys Leu His Leu  
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Glu Met Leu Ala Asp Gln Pro Arg Thr Thr Lys Tyr His Ser Val Ile  
20 25 30  
Leu Gln Asn Lys Glu Ser Leu  
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<210> 9

<211> 196

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 9

Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly  
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Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro Ser Cys  
20 25 30  
Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile Gln Val  
35 40 45  
Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile Arg Leu  
50 55 60  
Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp Pro Pro  
65 70 75 80  
Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser  
85 90 95  
Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro Arg Asp  
100 105 110  
Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg Pro  
115 120 125  
Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys  
130 135 140  
Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser Ser Leu  
145 150 155 160  
Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu  
165 170 175  
Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly Ser Arg  
180 185 190  
Pro Pro Cys Ser  
195